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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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EXAMINER	
BAUM, STUART F	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 04/09/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/014,927	BARTA ET AL.	
	Examiner	Art Unit	
	Stuart F. Baum	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *09 January 2004 and 05 December 2003*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *62-102* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *62-102* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *23 October 2001* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☒ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *2/15/2002*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

1. The amendment filed 1/9/2004 has been entered.

Claims 62-102 are pending.

2. Applicant's election without traverse of Group III, claims 23-24, 30-35, 39-40, 43-44, 47-48, 51-52, 55-56, and 59-60 filed 12/5/2003 is acknowledged.

Claims 1-61 have been canceled.

3. Claims 62-102 drawn to the subject matter of Group III, including SEQ ID NO:18 encoding SEQ ID NO:19 are examined in the present office action.

Specification

4. Objection is made to the specification for not incorporating SEQ ID NO's when referring to nucleic acid or amino acid sequences. 37 CFR 1.821(d) requires the use of the assigned sequence identifier (e.g. SEQ I.D. NO: X) in all instances where the description of a patent application discuss sequences. See for example pages 5, line 27 and page 6, line 1.

Foreign Priority

5. Acknowledgment is made of applicant's claim for foreign priority based on an application filed in Austria on 23 April 1999. It is noted, however, that applicant has not filed a certified copy of the Austrian application as required by 35 U.S.C. 119(b).

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

6. Claims 62-102 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The rejection includes dependent claims.

Claim 62 is indefinite in the recitation "atSRp30 protein". The sole designation of an amino acid sequence by "atSRp30 protein" is arbitrary and creates ambiguity in the claims. For example, the amino acid sequence in this application could be designated by some other arbitrary means, or the assignment of said name could be arbitrarily changed to designate a different amino acid sequence. If either event occurs, one's ability to determine the metes and bounds of the claim would be impaired. See *In re Hammack*, 427 F.2d 1378, 1382; 166 USPQ 204, 208 (CCPA 1970). Amendment of the claim to refer to a specific SEQ ID NO would obviate this rejection. All subsequent recitations of "atSRp30 protein" are also rejected.

In claim 62, the metes and bounds of "being derived from atSRp30 protein" have not been defined. Applicants have not specified what encompasses "being derived from atSRp30". Applicants have not disclosed how one measures the derivation of a protein from another protein and what parameters constitute a protein being derived from atSRp30 and what parameters constitute a protein not being derived from atSRp30.

In claim 65, the metes and bounds of "atSRp30 activity" have not been defined. Applicants have not defined the specific activity to which they are referring. The specification

does not explicitly state the function or activity of the atSRp30 protein, i.e., if the atSRp30 protein is involved in splicing mRNA, what sequence of mRNA does it bind to or splice?

Claim 65 is indefinite in the recitation "atSRp34/SR1 protein". The sole designation of an amino acid sequence by "atSRp34/SR1 protein" is arbitrary and creates ambiguity in the claims. For example, the amino acid sequence in this application could be designated by some other arbitrary means, or the assignment of said name could be arbitrarily changed to designate a different amino acid sequence. If either event occurs, one's ability to determine the metes and bounds of the claim would be impaired. See *In re Hammack*, 427 F .2d 1378, 1382; 166 USPQ 204, 208 (CCPA 1970). Amendment of the claim to refer to a specific SEQ ID NO would obviate this rejection.

In claim 65, lines 3 and 4, the phrase "to a truncated mRNA-isoform of an atSRp34/SR1 protein" is indefinite. It is not clear how atSRp30 protein expression leads to a truncated mRNA-isoform of an atSRp34/SR1 protein. Because of the indefiniteness of this phrase, this phrase will not be considered to further limit Applicants' invention.

Written Description

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claims 62, and 64-102 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably

convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to a recombinant nucleic acid molecule comprising a nucleic acid encoding a protein comprising more than 90% sequence identity with the sequence of amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19, or comprising a protein corresponding to or being derived from atSRp30 protein from a plant other than Arabidopsis, or a nucleic acid sequence which hybridizes to a nucleic acid molecule comprising SEQ ID NO:18 or its complement thereof, a promoter operably linked to said nucleic acid sequence, a cell, plant or plant cell transformed therewith, and method of changing the splicing properties of a plant or plant cell or method of changing the development of a plant or plant cell comprising transforming a plant with said nucleic acid molecule. For purposes of examination, the Office is interpreting the recitation "binds to" as recited for example in claim 62, line 8, to mean "hybridizes with" and the recitation "development behavior" as recited in claim 93, line 1, to mean "development".

Applicants disclose SEQ ID NO:18 and SEQ ID NO:19 (Sequence listing) but it is not stated that SEQ ID NO:18 encodes SEQ ID NO:19. Nowhere in the specification or sequence listing does Applicant disclose the start and stop codons of SEQ ID NO:18 that correspond with the protein disclosed in SEQ ID NO:19. Applicants do not reference SEQ ID NO:18 encoding SEQ ID NO:19 at all in the specification. In addition, the nucleic acid sequence disclosed in Figure 1A is 4073 base pairs longs while SEQ ID NO:18 is 4044 base pairs long.

Applicants also do not identify essential regions of SEQ ID NO:19, essential regions of atSRp30, nor do Applicants describe any polynucleotide sequences that hybridize to SEQ ID NO:18 and encode a protein with the same function as SEQ ID NO:19 or sequences that are 90%

sequence identical to amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19 and have the same function as SEQ ID NO:19. The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. See University of California v. Eli Lilly and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In summary, the court stated that a written description of an invention requires a precise definition, one that defines the structural features of the chemical genus that distinguishes it from other chemical structures. A definition by function does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. The court goes on to say, "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). Applicants fail to describe a representative number of polynucleotide sequences encoding a protein falling within the scope of the claimed genus of polynucleotides which hybridize to SEQ ID NO:18, or proteins that are derived from a atSRp30 protein from a plant other than Arabidopsis, or a polynucleotide that encodes a protein exhibiting 90% sequence identity to amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19. Applicants only describe a single genomic sequence of SEQ ID NO:18 and a protein sequence of SEQ ID NO:19. Furthermore, Applicants fail to describe structural features common to members of the claimed genus of polynucleotides. Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of congruence between SEQ ID NO:18, SEQ ID NO:19, and the claimed atSRp30 protein, and the lack of description of

the necessary elements essential for the protein of SEQ ID NO:19 or atSRp30, it remains unclear what features identify an Arabidopsis protein of SEQ ID NO:19 or atSRp30. Since the genus of proteins of SEQ ID NO:19 or atSRp30 have not been described by specific structural features, the specification fails to provide an adequate written description to support the breath of the claims.

Sequences that hybridize with SEQ ID NO:18 or encode a protein exhibiting 90% sequence identity to amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19 or proteins that are derived from atSRp30 encompass naturally occurring allelic variants, mutants of a protein, as well as sequences encoding proteins having no known splicing activity, of which Applicant is not in possession. Absent of such disclosure, one skilled in the art cannot determine the genus of sequences based upon the disclosure of the sequence of SEQ ID NO:18 and SEQ ID NO:19 with any certainty or predictability. Accordingly, the specification fails to provide an adequate written description to support the hybridization language or percent identity language as set forth in the claims. (See Written Description guidelines published in Federal Register/Vol. 66, No.4/Friday, January 5, 2001/Notices: p.1099-1111).

Enablement

8. Claims 62-102 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claims are drawn to a recombinant nucleic acid molecule comprising a nucleic acid sequence of SEQ ID NO:18, a nucleic acid sequence encoding SEQ ID NO:19, a nucleic acid sequence encoding a protein comprising more than 90% sequence identity with the sequence of amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19, or comprising a protein corresponding to or being derived from atSRp30 protein from a plant other than Arabidopsis, or a nucleic acid sequence which hybridizes to a nucleic acid molecule comprising SEQ ID NO:18 or its complement thereof, a promoter operably linked to said nucleic acid sequence, a cell, plant or plant cell transformed therewith, method of changing the splicing properties of a plant or plant cell or method of changing the development of a plant or plant cell comprising transforming a plant with said nucleic acid molecule. For purposes of examination, the Office is interpreting the recitation "binds to" as recited for example in claim 62, line 8, to mean "hybridizes with" and the recitation "development behavior" as recited in claim 93, line 1, to mean "development".

The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors. *In re Wands,* 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists a number of factors for determining whether or not undue experimentation would be required by one skilled in the art to make and/or use the invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claim.

Applicants disclose isolating a genomic clone, GatSRp30 from Arabidopsis and depositing said sequence as EMBL accession number AJ131214 (page 16, second paragraph)

and Applicants disclose that the sequence of GatSRp30 and the derived protein sequence are shown in Figure 1A (page 23, lines 25-26). Applicants disclose the constructs that were used to transform Arabidopsis were either the complete gene sequence as denoted pG30 or a cDNA sequence denoted as pC30 under the control of the 35S promoter (page 31 lines 25-28). Plants transformed with either the pG30 or pC30 construct exhibited phenotypic changes that comprised delayed flowering and when the plants were grown under short day conditions, the transformed plants exhibited a reduced apical dominance which resulted in a 'bushy' phenotype (page 34, lines 6-30).

The specification fails to provide guidance for the explicit sequence Applicants are using to encode the atSRp30 protein. The sequence deposited at EMBL is 5164 bp's long whereas the sequence in Figure 1A is 4073 bp's long, while SEQ ID NO:18 is 4044 bp's long. Applicants' claims are drawn to SEQ ID NO:18 and SEQ ID NO:19 but Applicants do not reference these sequences at all in the specification. Applicants have not disclosed the nucleotide sequence used in either pG30 or pC30 constructs. Applicants have not disclosed the start or stop codons associated with SEQ ID NO:18 that encode Applicants' amino acid sequence of SEQ ID NO:19, the purpose of which, demonstrates that Applicants are using a full length polypeptide sequence. It is noted from the Office's sequence search results of DNA's encoding SEQ ID NO:19 (a copy of which is included with the office action) that SEQ ID NO:18 does not encode the full length SEQ ID NO:19 polypeptide. Given this result, it is not clear what sequence Applicants used in the Examples to encode SEQ ID NO:19. In addition, given this result, Applicants have not taught how one skilled in the art use a plant transformed with a sequence that does not encode the full protein sequence of SEQ ID NO:19. In addition, Applicants fail to teach any nucleotide

sequence encoding a protein exhibiting 90% sequence identity with the sequence of amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19, or a nucleotide sequence that encodes a protein corresponding to or being derived from atSRp30 protein from a plant other than Arabidopsis, or a nucleotide sequence which hybridizes to a nucleotide sequence comprising SEQ ID NO:18 or its complement thereof, operably linked to any promoter, and cell, plant or plant cell transformation therewith.

The state-of-the-art is such that one of skill in the art cannot predict which nucleic acids that encode a protein exhibiting 90% sequence identity with amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19, or sequences that hybridize to SEQ ID NO:18, or sequences that encode a protein that is derived from atSRp30 from a plant other than Arabidopsis will encode a protein with the same activity as a protein encoded by SEQ ID NO:18. The prediction of protein structure from sequence data and, in turn, utilizing predicted structural determinations to ascertain functional aspects of the protein, is extremely complex, and the positions within the protein's sequence where amino acid substitutions can be made with a reasonable expectation of maintaining function are limited (Bowie et al, Science 247:1306-1310, 1990, see especially page 1306). Proteins may be sensitive to alterations in even a single amino acid in a sequence. For example, the replacement of a glycine residue located within the START domain of either the PHABULOSA or PHAVOLUTA protein receptor with either an alanine or aspartic acid residue, alters the sterol/lipid binding domain (McConnell et al, Nature 411 (6838):709-713, 2001, see especially page 710, left column, 2nd paragraph).

Applicants have not disclosed how one makes or isolates any of the sequences that are encompassed by Applicants' broad claims especially since it is not clear which sequence encodes

Applicants' invention. Applicants have not taught which regions of the respective polynucleotides can be used to amplify any of said polynucleotides or which regions can be used as a probe to isolate any of said polynucleotide sequences.

Applicants claims are directed to sequences that hybridize to SEQ ID NO:18. The state-of-the-art teaches isolating DNA fragments using stringent hybridization conditions, does not always select for DNA fragments whose contiguous nucleotide sequence is the same or nearly the same as the probe. Fourgoux-Nicol et al (1999, Plant Molecular Biology 40 :857-872) teach the isolation of a 674bp fragment using a 497bp probe incorporating stringent hybridization conditions comprising three consecutive 30 minute rinses in 2X, 1X and 0.1X SSC with 0.1% SDS at 65^0C (page 859, left column, 2^{nd} paragraph). Fourgoux-Nicol et al also teach that the probe and isolated DNA fragment exhibited a number of sequence differences comprising a 99bp insertion within the probe and a single nucleotide gap, while the DNA fragment contained 2 single nucleotide gaps and together the fragments contained 27 nucleotide mismatches. Taking into account the insertions, gaps and mismatches, the longest stretch of contiguous nucleotides to which the probe could hybridize consisted of 93bp of DNA (page 862, Figure 2).

Applicants have not provided examples or guidance for selecting a sequence out of the multitude of sequences that are encompassed by Applicants' broad claim language, that gives the expected results when transformed into a plant. Transforming plants with heterologous genes that are involved in plant development produce unpredictable results. Kano-Murakami et al (1993, FEBS 334:365-368) teach introducing the *Oryza sativa* homeobox 1 (OSH1) gene into tobacco. OSH1 is a rice homologue of the *Knotted-1* homeobox gene from maize and would be encompassed by Applicant's broad claim language. Kano-Murakami et al teach transgenic

tobacco plants comprising the OSH1 gene display a "range of phenotypes which include abnormalities in leaf and petal shape as well as stem height and number" (page 365, right column, 1st paragraph).

In the absence of guidance, undue trial and error experimentation would be required for one of ordinary skill in the art to screen through the multitude of non-exemplified sequences, either by using non-disclosed fragments of SEQ ID NO:18 as probes or by designing primers to undisclosed regions of SEQ ID NO:19 and isolating or amplifying fragments, subcloning the fragments, producing expression vectors and transforming plants therewith, in order to identify those, if any, that when over-expressed have splice factor activity and are able to change the splicing properties of a plant or plant cell and are able to change the time to flowering and apical dominance characteristics and encode a protein that is derived from atSRp30 from a plant other than Arabidopsis, or encodes a protein that exhibits 90% sequence identity to amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19.

Therefore, given the breadth of the claims; the lack of guidance and examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled.

Claim Rejections - 35 USC § 102

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

9. Claims 62, 64-67, 69-86, and 93-102 are rejected under 35 U.S.C. 102(b) as being anticipated by Meyerowitz et al (April, 1998, U.S. Patent Number 5,744,693).

The claims are drawn to a recombinant nucleic acid molecule, recombinant vector, and transgenic plant comprising a nucleic acid sequence that binds to a nucleic acid molecule

comprising SEQ ID NO:18, wherein the encoded protein is derived from atSRp30 protein from a plant other than Arabidopsis, wherein the encoded protein comprises atSRp30 activity, wherein the nucleic acid molecule is operably linked to a promoter, wherein the promoter is inducible, and method of changing the development of a plant comprising said nucleic acid molecule, wherein the change in development comprises a retardation of flower formation, wherein flower formation is retarded by at least 15% or 25% relative to a wild-type plant.

The office interprets the recitation "binds" to mean hybridize, and because Applicant has not specified conditions, the office interprets the conditions to be such that any nucleic acid will hybridize with SEQ ID NO:18. Because of the 112 2nd issues discussed above for "derived from atSRp30 protein", the office interprets this to read on any protein, and because of the 112 2nd issues discussed above for "atSRp30 activity", this limitation is not given any patentable weight.

Meyerowitz et al teach a tobacco plant transformed with a Brassica napus nucleic acid sequence operably linked to the 35S promoter (columns 12-14, Example 1). The transgenic tobacco plant produces flowers with retarded development comprising capelloid organs in the first and fourth whorls and staminoid organs in the second and third whorls (column 16, lines 16-19). Meyerowitz et al also teach inducible promoters (column 9, lines 3-16) and as such, Meyerowitz et al anticipate the claimed invention.

10. Claims 62, 66-68 and 76-77 are rejected under 35 U.S.C. 102(b) as being anticipated by Lazar (April, 1993, NCBI Accession Number M98340).

The claims are drawn to a recombinant nucleic acid molecule, or recombinant vector, comprising a nucleic acid sequence that binds to a nucleic acid molecule comprising SEQ ID

NO:18 under stringent conditions, wherein the nucleic acid molecule encodes a splice protein active in plants, and wherein the vector is biologically functional.

Lazar teaches a nucleic acid sequence that exhibits 63% identity (see enclosed sequence search result) to a nucleic acid sequence encoding amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19 wherein the sequence of Lazar would bind to SEQ ID NO:18 under stringent conditions and wherein the encoded protein is a splice protein and would be active in plants. For purposes of molecular biology, the vector comprising said sequence would be biologically functional and as such, Lazar anticipates the claimed invention. The Office interprets "stringent conditions" to be low stringency because Applicant has not specified any hybridization conditions and the Office interprets "biologically functional" to mean a vector that replicates in a host cell. The vector of Lazar would replicate in a host cell.

11. Claims 62-70, 73-78, 81-84, 87-90, and 93-100 are rejected under 35 U.S.C. 102(b) as being anticipated by Lopato et al (April 15, 1999, Genes & Development 13:987-1001; listed in IDS).

The claims are drawn to a recombinant nucleic acid molecule, method of changing the splicing properties of a plant or plant cell or method of changing the development of a plant or plant cell comprising a nucleic acid sequence encoding SEQ ID NO:19, a nucleic acid sequence encoding a protein comprising more than 90% sequence identity with the sequence of amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19, or a nucleic acid sequence which hybridizes to a nucleic acid molecule comprising SEQ ID NO:18 or its complement thereof, a promoter operably linked to said nucleic acid sequence, a cell, plant or plant cell transformed therewith.

For purposes of examination, the Office is interpreting the recitation "binds to" as recited for example in claim 62, line 8, to mean "hybridizes with" and the recitation "development behavior" as recited in claim 93, line 1, to mean "development".

Lopato et al teach a recombinant nucleic acid molecule comprising a nucleic acid sequence that is 99.4% sequence identical with SEQ ID NO:18 or that encodes a protein exhibiting at least 90% sequence identity with the sequence of amino acids 1 to 85 and 96 to 222 of SEQ ID NO:19, and the sequence would hybridize with SEQ ID NO:18 (page 989, Figure 1A and pages 998-999, Materials and methods), a recombinant vector comprising said nucleic acid sequence, and a plant transformed therewith, wherein the plant exhibits a changed development wherein the flowers exhibit at least 15%, or 25% retarded flower formation when compared to wild-type plants (page 994-995, section entitled "phenotypic changes in plants overexpressing atSRp30").

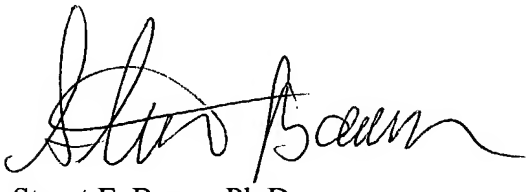
12. SEQ ID NO:18 encoding SEQ ID NO:19 and plant transformed therewith is free of the prior art, given the failure of the prior art to teach or reasonably suggest SEQ ID NO:18 encoding SEQ ID NO:19 and plant transformation therewith.

13. No claims are allowed.

14. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stuart F. Baum whose telephone number is 571-272-0792. The examiner can normally be reached on M-F 8:30-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on 571-272-0804. The fax phone number for the organization where this application or proceeding is assigned is (703) 872-9306.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.



Stuart F. Baum Ph.D.
Patent Examiner
Art Unit 1638
March 31, 2004